SEQUENCE LISTING

<110> Protalix Ltd.
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Lewkowicz, Ayala
Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<150> IL 155588
<151> 2003-04-27

<150> PCT/IL2004/000181
<151> 2004-02-24

<160> 14

<170> PatentIn version 3.5

<210> 1
<211> 22
<212> PRT
<213> Artificial sequence

<220>
<223> ER signal peptide

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Leu Ser Ser Ala Glu Phe
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<210> 2
<211> 7
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<213> Artificial sequence

<220>
<223> Vacuolar targeting signal from Tobacco chitinase A

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Asp Leu Leu Val Asp Thr Met
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<212> DNA
<213> Artificial sequence

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<223> Single strand DNA oligonucleotide

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<210> 4
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<212> DNA
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<223> Single strand DNA oligonucleotide

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<213> Artificial sequence

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ctcagaagac cagagggct 19

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<212> DNA
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<213> Homo sapiens

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gagagtacac gcagtgggcg acggatggag ctgagtatgg ggcccatcca ggctaatcac 180

acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga 240

tttggagggg ccatgacaga tgctgctgct ctcaacatcc ttgccctgtc acccccctgcc 300

caaaatttgc tacttaaatc gtacttctct gaagaaggaa tcggatataa catcatccgg 360

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<211> 497
<212> PRT
<213> Homo sapiens

<400> 8

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Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
35 40 45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
85 90 95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
130 135 140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
145 150 155 160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
165 170 175

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
180 185 190

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Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
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Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
    210                 215                 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
225                 230                 235                 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
                245                 250                 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
            260                 265                 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
        275                 280                 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
    290                 295                 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
305                 310                 315                 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
                325                 330                 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
            340                 345                 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
        355                 360                 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
    370                 375                 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
385                 390                 395                 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
                405                 410                 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
            420                 425                 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
        435                 440                 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
    450                 455                 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
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465 470 475 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg
485 490 495

Gln
497

<210> 9
<211> 338
<212> DNA
<213> Cauliflower mosaic virus

<400> 9
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ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180

acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240

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tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding the ER signal peptide

<400> 10
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gaattc 66

<210> 11
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11
gatcttttag tcgatactat g 21

<210> 12
<211> 167
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

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<221> misc_feature
<222> (162)..(162)
<223> n is a, c, g, or t

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agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120

tttataataa acaaagactt tgtcccaaaa acccccccc cngcaga 167

<210> 13
<211> 2186
<212> DNA
<213> Artificial sequence

<220>
<223> nucleic acid sequence encoding high mannose human glucocerebrosidase (GCD)

<220>
<221> misc_feature
<222> (2181)..(2181)
<223> n is a, c, g, or t

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ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180

acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240

tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300

tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac 360

aattaccaac aacaacaaac aacaaacaac attacaatta ctatttacaa ttacagtcga 420

gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt 480

ctcctatcat tatcctcggc cgaattcgcc cgcccctgca tccctaaaag cttcggctac 540

agctcggtgg tgtgtgtctg caatgccaca tactgtgact cctttgaccc cccgaccttt 600

cctgcccttg gtaccttcag ccgctatgag agtacacgca gtgggcgacg gatggagctg 660

agtatggggc ccatccaggc taatcacacg ggcacaggcc tgctactgac cctgcagcca 720

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gaaggaatcg gatataacat catccgggta cccatggcca gctgtgactt ctccatccgc 900

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<210> 14
<211> 526
<212> PRT
<213> Artificial sequence

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<223> High mannose human glucocerebrosidase (GCD)

<400> 14

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Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
130 135 140

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Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
145                 150                 155                 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
                165                 170                 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
            180                 185                 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
        195                 200                 205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
    210                 215                 220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
225                 230                 235                 240

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
                245                 250                 255

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
            260                 265                 270

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
        275                 280                 285

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
    290                 295                 300

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
305                 310                 315                 320

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
                325                 330                 335

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
            340                 345                 350

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
        355                 360                 365

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
    370                 375                 380

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
385                 390                 395                 400

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
                405                 410                 415

Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
            420                 425                 430
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Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
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Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
    450                 455                 460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
465                 470                 475                 480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
                485                 490                 495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
            500                 505                 510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
        515                 520                 525
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